

(i) APPLICANT: TZAHY ARAZI, YOEL MOSHE SHIBOLETH
AND AMIT GAL-ON

(ii) TITLE OF INVENTION: VECTORS FOR EXPRESSING HETEROLOGOUS

AT THE AMINO-TERMINUS OF POTYVIRUS COAT

Protein, methods for use thereof, plantS infected with same and methods of vaccination using same

(iii) NUMBER OF SEQUENCES: 33

(iv) CORRESPONDENCE ADDRESS:

(A)	ADDRESSEE:	Mark M. Friedman C/O Mr. Bill Polkinghorn Discovery Dispatch
(II)	STREET:	9003 Florin Way
(C)	CITY:	Upper Marlboro
(D)	STATE:	Maryland
(E)	COUNTRY:	United States of America
(F)	ZIP:	20772

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
(B) COMPUTER: Twinhead* Slimnote-890TX
(C) OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
(D) SOFTWARE: Word for Windows version 2.0 converted to
an ASCII file

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: XXX
(B) FILING DATE: XXX
(C) CLASSIFICATION: XXX

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/253,136
(B) FILING DATE: 28 November, 2000
(C) APPLICATION NUMBER:
(D) FILING DATE:
(V) APPLICATION NUMBER:
(F) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Friedman, Mark M.
(B) REGISTRATION NUMBER: 33,883
(C) REFERENCE/DOCKET NUMBER: 1686/4

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 972-3-5625553
(B) TELEFAX: 972-3-5625554
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

```
(A)      LENGTH:      837
(B)      TYPE:        nucleic acid
(C)      STRANDEDNESS: double
(D)      TOPOLOGY:    linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCAGGCCTACT	AGCCAACTGT	GGCAGATGCT	GGAGCTACAA	AGAAAGATAA	50
AGAAGATGTAC	AAAGCGAAAA	ACAAGGACGT	TACAGGCTCC	GGCTCAGGTG	100
AGAAACACAGT	AGAGCGTGTCT	ACGAAGGACA	AGGATGTGAA	TGCTGGTCTT	150
CATGGGAAAA	TTGTGCGCGC	TCTTTCGAAG	ATCACAAAGA	AAATGTCATT	200
GCCACGCGTG	AAAGGAAATG	TGATACTCGA	TATTGATCAT	TTGCTGGAAT	250
ATAAACCGGA	TCAAATGTGAG	TTATATAACA	CACGAGCGTC	TCATCAGCAG	300
TTCGCCTCTT	GGTTTCAACCA	GGTTTAAGAC	GAATATGATT	TGAACAGCAG	350
ACAGATGGGA	GTTGTAATGA	ATGGTTTCAT	GGTTTGCTGC	ATTGAGAATG	400

GCACTTCACC CGACATTAAT GGAGTGTGGG TTATGATGGA CGGAAATGAG 450
 CAAGTTGAGT ATCCCTTGAA ACCAATAGTT GAAAATGCAA AGCCAACGCT 500
 GCGGCAAATA ATGCATCATT TTTCAGATGC AGCGGAGGCA TATATAGAGA 550
 TGAGAAATGC AGAGGCACCA TACATGCCGA GGTATGGTTT GCTTCGAAAC 600
 CTACGGGATA GGAGTTTAGC ACGATATGCT TTTGATTCTT ATGAAGTCAA 650
 TTCTAAACT CCTGAAAGAG CCCGCGAAGC TGTTGCGCAG ATGAAAGCAG 700
 CAGCTCTTAG CAATGTTTCT TCAAGTTGT TTGGCCTTGA TGGAAATGTT 750
 GCCACCACTA GCGAAGACAC TGAACGGCAC ACTGCACGTG ATGTTAATAG 800
 AAACATGCAC ACCTTACTAG GTGTGAATAC AATGCAG 837

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Gly Thr Gln Pro Thr Val Ala Asp Ala Gly Ala Thr Lys Lys
 5 10 15
 Asp Lys Glu Asp Asp Lys Gly Lys Asn Lys Asp Val Thr Gly Ser
 20 25 30
 Gly Ser Gly Glu Lys Thr Val Ala Ala Val Thr Lys Asp Lys Asp
 35 40 45
 Val Asn Ala Gly Ser His Gly Lys Ile Val Pro Arg Leu Ser Lys
 50 55 60
 Ile Thr Lys Lys Met Ser Leu Pro Arg Val Lys Gly Asn Val Ile
 65 70 75
 Leu Asp Ile Asp His Leu Leu Glu Tyr Lys Pro Asp Gln Ile Glu
 80 85 90
 Leu Tyr Asn Thr Arg Ala Ser His Gln Gln Phe Ala Ser Trp Phe
 95 100 105
 Asn Gln Val Lys Thr Glu Tyr Asp Leu Asn Glu Gln Gln Met Gly
 110 115 120
 Val Val Met Asn Gly Phe Met Val Trp Cys Ile Glu Asn Gly Thr
 125 130 135
 Ser Pro Asp Ile Asn Gly Val Trp Val Met Met Asp Gly Asn Glu
 140 145 150
 Gln Val Glu Tyr Pro Leu Lys Pro Ile Val Glu Asn Ala Lys Pro
 155 160 165
 Thr Leu Arg Gln Ile Met His His Phe Ser Asp Ala Ala Glu Ala
 170 175 180
 Tyr Ile Glu Met Arg Asn Ala Glu Ala Pro Tyr Met Pro Arg Tyr
 185 190 195
 Gly Leu Leu Arg Asn Leu Arg Asp Arg Ser Leu Ala Arg Tyr Ala
 200 205 210
 Phe Asp Phe Tyr Glu Val Asn Ser Lys Thr Pro Glu Arg Ala Arg
 215 220 225
 Glu Ala Val Ala Gln Met Lys Ala Ala Ala Leu Ser Asn Val Ser
 230 235 240
 Ser Arg Leu Phe Gly Leu Asp Gly Asn Val Ala Thr Thr Ser Glu
 245 250 255
 Asp Thr Glu Arg His Thr Ala Arg Asp Val Asn Arg Asn Met His
 260 265 270
 Thr Leu Leu Gly Val Asn Thr Met Gln
 275 279

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATTTCTTT CACGCGTGGC 20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCACACCATC ACCATCACCA T

21

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser His His His His His His
 5 7

(2) INFORMATION FOR SEQ ID NO:6:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGCTGCAGT CACACCATCA CCATCACCAT TCAGGCACTC AGCCAACTGT 50
 GGC 53

(2) INFORMATION FOR SEQ ID NO:7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGCTGCAGT CACACCATCA CCATCACCAT GATACTGGAG CTACAAAGAA 50
 AGAAG 55

(2) INFORMATION FOR SEQ ID NO:8:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCAGCATCAG AGCAGAAGCT CATTTCAGAG GAGGATCTCG GATCC 45

(2) INFORMATION FOR SEQ ID NO:9:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 Ser Ala Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Ser
 5 10 15

(2) INFORMATION FOR SEQ ID NO:10:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGCTGCAGT CAGCATCAGA GCAGAAGCTC ATTTTCAGAGG AGGATCTCGG 50
 ATCCTCAGGC ACTCAGCCAA CTGTGGC 77

(2) INFORMATION FOR SEQ ID NO:11:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAGCTGCAGT CAGCATCAGA GCAGAAGCTC ATTTTCAGAGG AGGATCTCGG 50
 ATCCGATACT GGAGCTACAA AGAAAGATAA AG 82

(2) INFORMATION FOR SEQ ID NO:12:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: Single

00063754.002704

(2) INFORMATION FOR SEO ID NO:27:

CAGCTGCAGT CCAAGAAAGA CAAAGAAGAT GACAAAG

37

TCCATTATTA ATTCGAAAA GTTG 24

Ser Ile Ile Asn Phe Glu Lys Leu

5 8

CAGCTGCAGT CCATTATTAA TTTCGAAAAG TTGTCAGGCA CTCAGCCAAC 50
TGTGGC 56

CAGCTGCAGT CCGAGAAAAC AGTGGCAGCT GTC

33

AGCTCCATAC ATAGCTGAGA CA 22

TGGTTGAACC AAGAGGCGAA 20